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# 11/108 1600  
2/27/02

RAW SEQUENCE LISTING

DATE: 01/04/2002

PATENT APPLICATION: US/09/662,128A

TIME: 14:47:49

Input Set : A:\197330US0.ST25.txt

Output Set: N:\CRF3\01042002\I662128A.raw

ENTERED

3 <110> APPLICANT: MIYAGAWA, SHUJI  
4 OKABE, MASARU  
6 <120> TITLE OF INVENTION: MODIFIED CRE RECOMBINASE GENE FOR MAMMALS  
8 <130> FILE REFERENCE: 197330US0  
10 <140> CURRENT APPLICATION NUMBER: 09/662,128A  
11 <141> CURRENT FILING DATE: 2000-09-14  
13 <150> PRIOR APPLICATION NUMBER: JP11-264364  
14 <151> PRIOR FILING DATE: 1999-09-17  
16 <160> NUMBER OF SEQ ID NOS: 6  
18 <170> SOFTWARE: PatentIn version 3.0  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 1050  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Artificial Sequence  
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26 <221> NAME/KEY: CDS  
27 <222> LOCATION: (1)..(1050)  
29 <220> FEATURE:  
30 <221> NAME/KEY: misc\_feature  
31 <222> LOCATION: ()..()  
32 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic dna  
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37 Met Pro Lys Lys Lys Arg Lys Val Ser Asn Leu Leu Thr Val His Gln  
38 1 5 10 15  
40 aac ctg ccc gcc ctg ccc gtg gac gcc acc agc gac gag gtg cgc aag 96  
41 Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser Asp Glu Val Arg Lys  
42 20 25 30  
44 aac ctg atg gac atg ttc cgc gac cgc cag gcc ttc agc gag cac acc 144  
45 Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala Phe Ser Glu His Thr  
46 35 40 45  
48 tgg aag atg ctg ctg agc gtg tgc cgc agc tgg gcc gcc tgg tgc aag 192  
49 Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys  
50 50 55 60  
52 ctg aac aac cgc aag tgg ttc ccc gcc gag ccc gag gac gtg cgc gac 240  
53 Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp  
54 65 70 75 80  
56 tac ctg ctg tac ctg cag gcc cgc ggc ctg gcc gtg aag acc atc cag 288  
57 Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala Val Lys Thr Ile Gln  
58 85 90 95  
60 cag cac ctg ggc cag ctg aac atg ctg cac cgc cgc agc ggc ctg ccc 336  
61 Gln His Leu Gly Gln Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro  
62 100 105 110  
64 cgc ccc agc gac agc aac gcc gtg agc ctg gtg atg cgc cgc atc cgc 384  
65 Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg  
66 115 120 125  
68 aag gag aac gtg gac gcc ggc gag cgc gcc aag cag gcc ctg gcc ttc 432

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69 Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys Gln Ala Leu Ala Phe
70      130      135      140
72 gag cgc acc gac ttc gac cag gtg cgc agc ctg atg gag aac agc gac      480
73 Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu Met Glu Asn Ser Asp
74 145      150      155      160
76 cgc tgc cag gac atc cgc aac ctg gcc ttc ctg ggc atc gcc tac aac      528
77 Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu Gly Ile Ala Tyr Asn
78      165      170      175
80 acc ctg ctg cgc atc gcc gag atc gcc cgc atc cgc gtg aag gac atc      576
81 Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile Arg Val Lys Asp Ile
82      180      185      190
84 agc cgc acc gac ggc ggc cgc atg ctg atc cac atc ggc cgc acc aag      624
85 Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys
86      195      200      205
88 acc ctg gtg agc acc gcc ggc gtg gag aag gcc ctg agc ctg ggc gtg      672
89 Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val
90      210      215      220
92 acc aag ctg gtg gag cgc tgg atc agc gtg agc ggc gtg gcc gac gac      720
93 Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp
94 225      230      235      240
96 ccc aac aac tac ctg ttc tgc cgc gtg cgc aag aac ggc gtg gcc gcc      768
97 Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala
98      245      250      255
100 ccc agc gcc acc agc cag ctg agc acc cgg gcc ctg gag ggc atc ttc      816
101 Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe
102      260      265      270
104 gag gcc acc cac cgc ctg atc tac ggc gcc aag gac gac agc ggc cag      864
105 Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys Asp Asp Ser Gly Gln
106      275      280      285
108 cgc tac ctg gcc tgg agc ggc cac agc gcc cgc gtg ggc gcc gcc cgc      912
109 Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg
110      290      295      300
112 gac atg gcc cgc gcc ggc gtg agc atc ccc gag atc atg cag gcc ggc      960
113 Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly
114 305      310      315      320
116 ggc tgg acc aac gtg aac atc gtg atg aac tac atc cgc aac ctg gac      1008
117 Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr Ile Arg Asn Leu Asp
118      325      330      335
120 agc gag acc ggc gcc atg gtg cgc ctg ctg gag gac ggc gac      1050
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128 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <221> NAME/KEY: misc_feature
132 <222> LOCATION: ()..()
133 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide

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135 &lt;400&gt; SEQUENCE: 2

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137 Met Pro Lys Lys Lys Arg Lys Val Ser Asn Leu Leu Thr Val His Gln
138 1 5 10 15
141 Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser Asp Glu Val Arg Lys
142 20 25 30
145 Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala Phe Ser Glu His Thr
146 35 40 45
149 Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp Ala Ala Trp Cys Lys
150 50 55 60
153 Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro Glu Asp Val Arg Asp
154 65 70 75 80
157 Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala Val Lys Thr Ile Gln
158 85 90 95
161 Gln His Leu Gly Gln Leu Asn Met Leu His Arg Arg Ser Gly Leu Pro
162 100 105 110
165 Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val Met Arg Arg Ile Arg
166 115 120 125
169 Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys Gln Ala Leu Ala Phe
170 130 135 140
173 Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu Met Glu Asn Ser Asp
174 145 150 155 160
177 Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu Gly Ile Ala Tyr Asn
178 165 170 175
181 Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile Arg Val Lys Asp Ile
182 180 185 190
185 Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His Ile Gly Arg Thr Lys
186 195 200 205
189 Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala Leu Ser Leu Gly Val
190 210 215 220
193 Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser Gly Val Ala Asp Asp
194 225 230 235 240
197 Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys Asn Gly Val Ala Ala
198 245 250 255
201 Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala Leu Glu Gly Ile Phe
202 260 265 270
205 Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys Asp Asp Ser Gly Gln
206 275 280 285
209 Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg Val Gly Ala Ala Arg
210 290 295 300
213 Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu Ile Met Gln Ala Gly
214 305 310 315 320
217 Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr Ile Arg Asn Leu Asp
218 325 330 335
221 Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu Asp Gly Asp
222 340 345 350
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 34
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence

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230 <220> FEATURE:
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: ()..()
233 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
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240 <210> SEQ ID NO: 4
241 <211> LENGTH: 29
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <221> NAME/KEY: misc_feature
247 <222> LOCATION: ()..()
248 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
251 <400> SEQUENCE: 4
252 ttcgtatagc atagattata cgaagttat 29
255 <210> SEQ ID NO: 5
256 <211> LENGTH: 29
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: ()..()
263 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
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271 <211> LENGTH: 21
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276 <221> NAME/KEY: misc_feature
277 <222> LOCATION: ()..()
278 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
281 <400> SEQUENCE: 6
282 cccaagaaga agaggaaggt g 21

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VERIFICATION SUMMARY

DATE: 01/04/2002

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Input Set : A:\197330US0.ST25.txt

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